American Journal of Infection Control ■■ (2017) ■■-■■

Contents lists available at ScienceDirect

American Journal of Infection Control

journal homepage: www.ajicjournal.org

Major Article

Characteristics of methicillin-resistant *Staphylococcus aureus* in patients on admission to a teaching hospital in Rio de Janeiro, Brazil

Fernanda Sampaio Cavalcante PhD [a,1], Marcos Vinicius Pinheiro MSc [b,1], Dennis de Carvalho Ferreira PhD [c,d], Celina Vieira da Cunha Guedes Alvarenga BBS [e], Ana Carolina Fonseca Guimarães BBS [e], Simone Aranha Nouér MD, PhD [b], Kátia Regina Netto dos Santos PhD [e,*]

[a] *Campus Macaé, Federal University of Rio de Janeiro, Macaé, Brazil*
[b] *School of Medicine, Federal University of Rio de Janeiro, Rio de Janeiro, Brazil*
[c] *School of Dentistry, Veiga de Almeida University, Rio de Janeiro, Brazil*
[d] *School of Dentistry, Estácio de Sá University, Rio de Janeiro, Brazil*
[e] *Institute of Microbiology, Federal University of Rio de Janeiro, Rio de Janeiro, Brazil*

Key Words:
MRSA
Hospital admission
Nasal colonization
Lineages

Background: Infections caused by methicillin-resistant *Staphylococcus aureus* (MRSA) are associated with greater mortality and morbidity; however, risk factors for community-acquired infections caused by MRSA have not been established. Therefore, community patients who are admitted to hospitals without the necessary contact precautions and are infected with community-acquired lineages eventually cause these lineages to spread to these settings. The aim of this study was to detect community-acquired lineages of MRSA in patients on admission to a Brazilian teaching hospital.

Methods: The antimicrobial susceptibility of the MRSA isolates from nasal swabs was evaluated as was the molecular characteristics of the staphylococcal cassette chromosome *mec* (SCC*mec*). The clonality was determined using pulsed-field gel electrophoresis and multilocus sequence type analysis.

Results: A total of 702 patients were evaluated between March 2012 and March 2013; 180 (25%) of them were colonized by *S aureus*, and 21 (3%) were MRSA. The SCC*mec* IV/USA1100/sequence type (ST) 30 was the predominant MRSA lineage (42.8%), followed by SCC*mec* IV/USA800/ST5 (23.8%).

Conclusions: The occurrence of MRSA colonization was very low, and only 1 patient from cardiac surgery developed an infection, which was caused by an SCC*mec* II/USA100/ST5 isolate. Screening for MRSA colonization on admission does not seem to be productive; however, for populations submitted to specific surgeries, active surveillance should be implemented.

BACKGROUND

Methicillin-resistant *Staphylococcus aureus* (MRSA) is an important cause of health care–associated (HCA) infections, causing a mortality rate of approximately 20%.[1] Isolates related to the Brazilian endemic clone/staphylococcal cassette chromosome *mec* (SCC*mec*) III/sequence type (ST) 239 lineage were responsible for 90% of the nosocomial MRSA isolates in Brazil in the late 1990s.[2] Over the last 2 decades, MRSA isolates carrying SCC*mec* IV have emerged in communities worldwide. Since 2004, the presence of community lineages, such as USA400 and USA1100 (Ocean Southwest Pacific Clone), have been described as causing nosocomial infections[3,4] in Brazil. Because risk factors for community-acquired infections because of MRSA have not been established,[5] these patients are admitted to hospitals without any contact precautions.

* Address correspondence to Kátia Regina Netto dos Santos, PhD, Laboratório de Infecção Hospitalar, Departamento de Microbiologia Médica, Instituto de Microbiologia Paulo de Góes, Universidade Federal do Rio de Janeiro, CCS, Bloco I, Sala 010, Rio de Janeiro, CEP: 21941-590, Brazil.

E-mail address: santoskrn@micro.ufrj.br (K.R.N. dos Santos).

Funding/support: Supported by Brazilian grants from Fundação Carlos Chagas Filho de Amparo à Pesquisa do Estado do Rio de Janeiro, Conselho Nacional de Desenvolvimento Científico e Tecnológico, Coordenação de Aperfeiçoamento de Pessoal de Nível Superior, Fundação Universitária José Bonifácio, and Programa de Núcleos de Excelência.

Conflicts of interest: None to report.

[1] The authors contributed equally to this work.

0196-6553/
http://dx.doi.org/10.1016/j.ajic.2017.06.003

Therefore, community-acquired lineages eventually spread throughout these settings.

Most of the colonized patients act as silent reservoirs for further transmission.[6] The active surveillance of this pathogen can reduce infection rates and be cost beneficial.[7] Therefore, several strategies have been developed to prevent MRSA dissemination, including active screening on patient admission at health care institutions.[8] Risk factors associated with nosocomial acquisition of MRSA are well recognized. However, it is unclear whether community-acquired MRSA colonization is associated with some of these risk factors or a different set of risk factors.[9] In this study, we aimed primarily to detected patients colonized by MRSA on admission to a teaching hospital over a 1-year period. Furthermore, we addressed the molecular and phenotypic characteristics of these isolates and described the clinical aspects associated with the patients.

MATERIALS AND METHODS

This observational prospective study was carried out from March 2012-March 2013 at the Hospital Universitário Clementino Fraga Filho, a tertiary care public teaching hospital in Rio de Janeiro, Brazil. The hospital has 280 beds, with approximately 1,200 patients admitted per month to the general medical, surgical, and infectious disease wards, and to the dialysis, hematology, oncology, and organ transplantation units. This study was approved by the research ethics committee (no. 159/07). Clinical data of patients were taken from the hospital records. The study variables were defined as age, sex, body mass index, comorbidities, Charlson comorbidity index score, cause of admission, and outcome.

Patients ≥18 years old and who were admitted within 72 hours at any of the hospital units were considered for the study. Patients with altered levels of consciousness, previously colonized by MRSA, or with other causes to inhibit the sample collection (eg, nasal tubes, declined to participate) were excluded. The selection of the patients for this study followed a randomization strategy to reduce selection bias and to guarantee a representativeness of the patients. The selection process aimed to meet the premise that each individual admitted to the hospital had a chance to be chosen as an example of the study population. To guarantee this probability, a simple sampling was performed where a draw of 10 patients was carried out each day. However, if the patient selected could not participate, the subsequent patient on the list was chosen.

One nasal swab from each patient was collected. Specimens were cultured in mannitol salt agar (Oxoid, Basingstoke, UK) and the *S aureus* isolates were characterized by using standardized tests.[10] Screening for MRSA was performed using a cefoxitin disk (30 μg) (CECON, São Paulo, Brazil).[11] The SCC*mec* types were accessed by multiplex polymerase chain reaction for MRSA isolates.[12] Detection of *PVL* genes was carried out by polymerase chain reaction.[13] Clonal relationship was determined by pulsed field gel electrophoresis,[2] and the multilocus sequence typing was performed for representative MRSA isolates.[14]

RESULTS

During the study period, 702 patients were included. The mean age was 48.4 ± 16.12 years old, body mass index was 26.5 kg/m^2, and 51.7% were women. The Charlson comorbidity index score mean was 0.43 (range, 0-6), and 76.8% of the patients had no comorbidities. Most patients were admitted for a surgical procedure (70%), and all of them were screened within 48 hours after hospitalization. One patient died because of bladder neoplasia, and all others were discharged. Also, only 1 patient developed further infection by MRSA.

Among the 180 (25.6%) patients who carried *S aureus* isolates, 21 (3% of all patients; 11.7% of all *S aureus* isolates) were colonized by MRSA (Table 1), and they had the same median age as the others (median, 48.3 years; range, 19-72) (Table 2). Among the MRSA patients, 47.6% had some comorbidities; systemic arterial hypertension was the most common (80%). In relation to the presence of an underlying disease, there was no statistically significant difference among MRSA and methicillin-susceptible *S aureus* patients.

Table 1
General characteristics of *Staphylococcus aureus* isolates from 702 patients on admission to a Brazilian teaching hospital, between March 2012 and March 2013

Characteristic	n (%)
S aureus total	180 (25.6)
MSSA	159 (88.3)
MRSA	21 (11.7)
SCC*mec* II	3 (14.3)
SCC*mec* III	2 (9.5)
SCC*mec* IV	15 (71.4)
Nontypeable cassette	1 (4.8)

MRSA, methicillin-resistant *S aureus*; *MSSA*, methicillin-susceptible *S aureus*; *SCCmec*, staphylococcal cassette chromosome *mec*.

Molecular analysis revealed that 15 (71.4%) of the MRSA isolates carried SCC*mec* IV, 3 (14.3%) had SCC*mec* II, 2 (9.5%) had SCC*mec* III, and 1 (4.8%) isolate presented a nontypeable cassette (*mec* complex and *ccr* gene absent) (Table 1). The SCC*mec* IV isolates were associated with the following lineages: USA1100/ST30 (8 isolates), USA800/ST5 (5 isolates), USA300 (1 isolate), and 1 isolate presented a nondetermined clonality, but multilocus sequence typing analysis revealed ST30 (Table 2). All the SCC*mec* II and III isolates were related to the USA100/ST5 and Brazilian endemic clone/ST239 lineages, respectively. The isolate with the nontypeable cassette belonged to the ST2140 lineage. *PVL* genes were detected in 6 (28.6%) of the MRSA isolates, all carrying the SCC*mec* IV, and 4 of them were associated with the USA1100/ST30 lineage, and the others were related to the USA300/ST8 and USA800/ST5 lineages.

All colonized patients were followed until discharge and for at least 2 years at the outpatient department. One patient developed an infection because of MRSA. This patient was submitted to cardiac surgery, performed 6 days after hospitalization. The MRSA identification of this patient was not available before the surgery; therefore, the infection control routine of decolonization or changing in antimicrobial prophylaxis could not be done. Eighteen days after myocardial revascularization, the patient developed bacteremia. Molecular analysis of the isolates recovered from the nasal swab on admission and blood cultures revealed that both belonged to the same lineage: SCC*mec*II/USA100/ST5. The patient was treated with teicoplanin successfully.

DISCUSSION

S aureus is still the main pathogen involved in HCA infections; therefore, knowledge concerning the magnitude of MRSA colonization among patients is important to plan the control of this pathogen. In this study, 3% of the 702 patients without any classical risk factors for MRSA were colonized. A similar rate was found by Otter el al,[15] who reported MRSA in 2% of 28,892 patients on admission to a tertiary care hospital in the United Kingdom. However, Santos et al[16] conducted a similar study in Brazil, and found 5.9% of patients had MRSA isolates after screening 297 patients admitted to an intensive care unit and an emergency room in Porto Alegre, in the south of Brazil. Although most studies show that there is an association between underlying diseases and MRSA,[17] most of the patients evaluated in our study did not have any chronic diseases and the mean Charlson comorbidity index score was very low, probably because most of them (70%) were admitted for elective surgeries.