The nares as a CA-MRSA reservoir in the healthy elderly

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ABSTRACT

Introduction: The frequency of methicillin-resistant Staphylococcus aureus (MRSA) has increased in the community. This study evaluated the prevalence of MRSA and community-acquired (CA)-MRSA in 120 healthy elderly. Methods: The MRSA were evaluated for the presence of the IS256, mecA, agr, icaA, icaD, fnbB, and pvl genes with PCR. Results: Frequency of S. aureus and MRSA colonization was 17.8% and 19%, respectively. CA-MRSA isolate showed SCCmec IV, fnbB+, and icaD+. Conclusions: CA-MRSA was detected, with genotype determined as SCCmec type IV/IS256-/fnbB+/icaA-/icaD-/bbp-/agr-/pvl-, characterizing this population as a possible reservoir of this organism in the community.

Keywords: CA-MRSA. Elderly. Reservoir.
**Table 1** shows that a total of 21 *S. aureus* isolates were recovered from the nares of 120 subjects, and the nasal carriage rate was 17.8% (21/118 nares colonized by *Staphylococcus* spp.). The disk diffusion method characterized 19% (4/21) of the isolates as MRSA and 50% (2/4) with MIC ≥4mg/L (only one multidrug resistance isolate). In total, 50% of the MRSA showed multidrug resistance with resistance to erythromycin, rifampicin, and clindamycin. On the other hand, all strains of MRSA were susceptible to ciprofloxacin, gentamicin, amikacin, tetracycline, and sulfamethoxazole/trimethoprim.

The presence of the *mecA* gene was confirmed in two isolates with MIC ≥4mg/L, which carried SCCmec type II and IV, respectively. Despite not being tested, it is possible that the other two samples detected in our search (*mecA*-, cefoxitin resistant) have the new homologous variant *mecC* that has 70% identity with *mecA*. The *mecC* gene is not detected with the PCR method established for the detection of *mecA*; consequently, isolates harboring this new variant can be misidentified and reported as methicillin-susceptible *S. aureus*\(^{(13)}\). The CA-MRSA isolated showed the following genotypic profile: SCCmec type IV/IS256\(/fnbB'/icaA'/icaD'/bhp/agr2/bap/pvl\). None of the elderly participants colonized with MRSA had previous hospitalization or had undergone any hospital procedure in the 12 months before the study.

The majority of studies conducted to evaluate asymptomatic carriage of MRSA have been performed in individuals in the community who have had contact with a hospital environment. Studies of epidemiological surveillance for CA-MRSA carriage in healthy subjects are rare in Brazil. This study provides the first description of CA-MRSA with genotypic profile in this population.

In our study, we also detected a strain carrying the SCCmec type II. The epidemiology of MRSA is a dynamic process that brings to light the blurring of the limits between the community and hospital\(^{(14)}\). According to the literature, the strains carrying SCCmec type II are associated with clinical isolates recovered from the hospital\(^{(2)}\). One possible explanation for this is that the elderly participants have probably had previous contact with someone who was recently hospitalized. Additionally, previous contamination of the environment is also considered an important reservoir of microorganisms\(^{(14)}\).

Although we have found only one SCCmec type IV *pvl*, the frequency of nares colonized by MRSA (19%, 4/21) were similar to those found in Mexico City, where 12.6% of *S. aureus* carriers were colonized with MRSA, both rates higher than those reported in the United States (1.5%)\(^{(3)}\).

We compared PCR assays for the detection of the methicillin-resistance gene with classical methods in this study. The two isolates initially classified as methicillin-resistant based on disk diffusion showed discrepant results when tested with the E-test\(^e\) and PCR. Investigators have reported that the conventional susceptibility testing methods, mainly the diffusion
Molecular epidemiology studies have highlighted the global spread of different MRSA clones. HA-MRSA may have a hidden reservoir in the community just as the CA-MRSA has one in health services. This increases the need to monitor such clones. Although our isolates were not clonally typed, the presence of CA-MRSA and HA-MRSA genotypes colonizing healthy elderly participants in a multisport center emphasizes the risk of cross-transmission. The presence of different MRSA clones in this group could not be determined in our study, but warrants additional research.

In this study of healthy elderly people in Minas Gerais, Brazil, we detected the prevalence of MRSA, including CA-MRSA, among S. aureus carriers. The importance of CA-MRSA colonization as a risk factor for cross-transmission in the community must be further analyzed.

ACKNOWLEDGMENTS

The authors would like to thank Dra Kátia Regina Netto dos Santos (Institute of Microbiology Paulo de Goés, Universidade Federal do Rio de Janeiro-UFRJ) who kindly provided the control strain Clone Southwest Pacific.

CONFLICT OF INTEREST

The authors declare that there is no conflict of interest.

FINANCIAL SUPPORT

The authors would like to thank Fundação de Amparo à Pesquisa do Estado de Minas Gerais (FAPEMIG).

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